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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/938,342 DATE: 09/18/2001
TIME: 11:15:26

Input Set : A:\198069.txt
Output Set: N:\CRF3\09182001\I938342.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Inze, Dirk
6 Segers, Gerda
7 De Veylder, Lieven
8 Mironov, Vladimir
10 (ii) TITLE OF INVENTION: METHOD AND MEANS FOR MODULATING
11 PLANT CELL CYCLE PROTEINS AND THEIR USE IN PLANT
12 CELL GROWTH AND CONTROL
14 (iii) NUMBER OF SEQUENCES: 4
C--> 16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Nixon Peabody LLP
18 (B) STREET: 990 Stewart Avenue
19 (C) CITY: Garden City
20 (D) STATE: New York, New York
C--> 21 (E) ZIP: 11530
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/938,342
C--> 31 (B) FILING DATE: 24-Aug-2001
32 (C) CLASSIFICATION:
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: EP PCT/EP98/01522
36 (B) FILING DATE: 13-MAR-1998
37 (A) APPLICATION NUMBER: EP 97.200.765.2
38 (B) FILING DATE: 14-MAR-1997
40 (2) INFORMATION FOR SEQ ID NO: 1:
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 454 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
46 (D) TOPOLOGY: linear
48 (ii) MOLECULE TYPE: cDNA
50 (iii) HYPOTHETICAL: NO
52 (vi) ORIGINAL SOURCE:
53 (A) ORGANISM: Arabidopsis thaliana
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION:15..276
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 CCTCTGAGAG AGAA ATG GGT CAG ATC CAA TAC TCC GAG AAA TAC TTC GAT 50
62 Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp
63 1 5 10

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65 GAC ACT TTC GAA TAC AGG CAC GTC GTT CTT CCT CCT GAA GTC GCT AAA      98
66 Asp Thr Phe Glu Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys
67      15      20      25
69 CTT CTT CCA AAG AAT CGT CTT CTC TCC GAA AAC GAA TGG CGA GCG ATA      146
70 Leu Leu Pro Lys Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile
71      30      35      40
73 GGA GTG CAG CAA AGC CGC GGA TGG GTA CAT TAC GCG GTT CAT CGA CCT      194
74 Gly Val Gln Gln Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro
75      45      50      55      60
77 GAG CCG CAC ATA ATG CTA TTC AGG AGG CCT CTT AAC TAT CAG CAG CAG      242
78 Glu Pro His Ile Met Leu Phe Arg Arg Pro Leu Asn Glu Trp Arg Ala Gln
79      65      70      75
81 CAG GAG AAT CAA GCT CAG AAC ATG CTT GTT AAG T GAATCATTAT      286
82 Gln Glu Asn Gln Ala Gln Asn Met Leu Val Lys
83      80      85
85 CATCACCTGCA GTAAGAATGT TATATGCAAC AATTCATGTA GTATTGGTTT ATGTTTCTTG      346
87 TAAACATGGT TTGAATCTTT GTGGTTATGG ATGAATATGT CAGAGTTGGT TTGTTGAACA      406
89 ACTTCTATGT AATGTTAGTC TTGTTCTCAA TGTCATCTTC TGCTTCTC      454
92 (2) INFORMATION FOR SEQ ID NO: 2:
93 (i) SEQUENCE CHARACTERISTICS:
94 (A) LENGTH: 696 base pairs
95 (B) TYPE: nucleic acid
96 (C) STRANDEDNESS: double
97 (D) TOPOLOGY: linear
98 (ii) MOLECULE TYPE: DNA (genomic)
99 (iii) HYPOTHETICAL: NO
100 (vi) ORIGINAL SOURCE:
101 (A) ORGANISM: Arabidopsis thaliana
102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
103
109 ATGGGTCAGA TCCAAATCTC CGAGAAATAC TTCGATGACA CTTTCGAATA CAGGTAAGGC      60
111 TCTTCAATCT CGCTCTCTCT TCCTCCAAAT TTCACCTCTCA CTTCTCTAAT CGTAATCGAT      120
113 CGATACAGGC ACGTCGTCTC TCCTCCGAA GTCCGCTAAAC TCTTCCAAA GAATCGTCTT      180
115 CTCTCCGAAG TAAGTTTTTT TCCGCATTGT TCTCTGATTT CTGATTCTAA ATCTTTCGAT      240
117 TAGATCATCG AAGACTATGA AAATTTGTGT CTCTTAAGAA ATTAAGTTTG GGAATAATCG      300
119 AAAAAAGAGAT CTTTTAGGTT TAGGATTGTA ATCTTTGCTC TGAATCCAAA TTGCAACTGT      360
121 TACGATTTTG AATCTTGTCT TTGGGATTTT GTAAGGTTTA GTGATAAAGA GATTTTAGAC      420
123 ATTTGTGTGT TGCAATCTCT TCAATGTTGT ATTGATTGGT GGTGATGGTA AAAATGTTTG      480
125 GAATTTGCAA GAACGAATGG CGAGCGATAG GAGTGCAGCA AAGCCGCGGA TGGGTACATT      540
127 ACGCGGTGCA TCGACCTGAG CCGCACATAA TGCTATTACG GAGGCGCTCT AACTATCAGC      600
129 AGCAGCAGGA GAATCAAGCT CAGAACATGC TTGTTAAGTG AATCATTATC ATCACTCGAG      660
131 TAAGATGTTT ATATGCAACA GATCTATGAG TATTGG      696
133 (2) INFORMATION FOR SEQ ID NO: 3:
134 (i) SEQUENCE CHARACTERISTICS:
135 (A) LENGTH: 87 amino acids
136 (B) TYPE: amino acid
137 (C) STRANDEDNESS:
138 (D) TOPOLOGY: linear
139 (ii) MOLECULE TYPE: peptide
140 (vi) ORIGINAL SOURCE:

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144      (A) ORGANISM: Arabidopsis thaliana
146  (ix) FEATURE:
147      (A) NAME/KEY: Peptide
148      (B) LOCATION:1
150  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
152  Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp Asp Thr Phe Glu
153      1          5          10          15
155  Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys Leu Leu Pro Lys
156      20          25          30
158  Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile Gly Val Gln Gln
159      35          40          45
161  Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro Glu Pro His Ile
162      50          55          60
164  Met Leu Phe Arg Arg Pro Leu Asn Tyr Gln Gln Gln Gln Glu Asn Gln
165      65          70          75          80
166  Ala Gln Asn Met Leu Val Lys
167      85
170  (2) INFORMATION FOR SEQ ID NO: 4:
172  (i) SEQUENCE CHARACTERISTICS:
173      (A) LENGTH: 72 amino acids
174      (B) TYPE: amino acid
175      (C) STRANDEDNESS:
176      (D) TOPOLOGY: linear
178  (ii) MOLECULE TYPE: peptide
180  (vi) ORIGINAL SOURCE:
181      (A) ORGANISM: Arabidopsis thaliana
183  (ix) FEATURE:
184      (A) NAME/KEY: Peptide
185      (B) LOCATION:1
187  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
189  Met Gly Gln Ile Gln Tyr Ser Glu Lys Tyr Phe Asp Asp Thr Phe Glu
190      1          5          10          15
192  Tyr Arg His Val Val Leu Pro Pro Glu Val Ala Lys Leu Leu Pro Lys
193      20          25          30
195  Asn Arg Leu Leu Ser Glu Asn Glu Trp Arg Ala Ile Gly Val Gln Gln
196      35          40          45
198  Ser Arg Gly Trp Val His Tyr Ala Val His Arg Pro Glu Pro His Ile
199      50          55          60
201  Met Leu Phe Arg Arg Pro Leu Asn
202      65          70

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L:16 M:220 C: Keyword misspelled or invalid format, [(1v) CORRESPONDENCE ADDRESS:]
L:21 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]